

FIG. 1 - 1

Set I.

V _H 4-39		D6-13		J _H 5		
C	A R H/Q			N W F D		
TGT	GCG AGA CA			AAC TGG TTC GAC		
C	A S S R	G	<u>Y</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>Y</u> <u>TAC</u>			
TGT	GCG AGC TCC AGA	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				
C	A R H L	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				CLL039
TGT	GCG AGA CAT CTG	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				CLL057
C	A R R F	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				CLL114
TGT	GCG AGA CGG TTC	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				
C	A R S T	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				CLL202
TGT	GCG AGG TCG ACC	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				
C	A R Q A	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				CLL209
TGT	GCG AGA CAA GCT	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				
C	A R H E	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				
TGT	GCG AGA CAT GAG	<u>G</u> <u>G</u> <u>G</u> <u>TAT</u> <u>AGC</u> <u>S</u> <u>S</u> <u>S</u> <u>W</u> <u>TGG</u> <u>TAC</u>				Y09249 immunocyto

FIG. 1 - 2

Set II.

V _H 4-34		D5-5		J _H 6	
C A R G	V D T A M V	Y Y Y Y		AT TAC TAC TAC	
TGT GCG AGA GG	GTG GAT ACA GCT ATG GTT AC				
C A R G	G D T P T I R R Y Y			C _{LL} 183	
TGT GCG AGA GGA TAC GGG GAT ACA CCT ACC ATT AGA AGA TAC TAT	A D T P V F R R Y Y			C _{LL} 240	
C A R G	G D T P M L K R Y Y			C _{LL} 342	
TGT GCG AGA GGC TGG GGG GAT ACA CCT ATG CTT AAA AGA TAC TAC	P D T P M V R R Y Y			AF087422	
C A R A GCA TAC CCG GAT ACA CCT ATG GTC AGG AGG TAC TAC	D V I K R Y Y			C _{LL} 4B ¹	
C A R G	F P D T I K R Y Y			AJ239333	
TGT GCG AGA GGC TTC CCG GAT ACA GAT GTG ATT AAG CGC TAC TAC				C _{LL} ID 47 ²	

3/16

FIG. 1 - 3

Set Via.

V _H 1-02				D6-19				J _H 4				
C	A	R	D/E					Y	F	D	Y	
TGT	GCG	AGA	GA					AC	TAC	TTT	GAC	TAC
	<u>GG</u>	<u>GTA</u>	<u>TAG</u>	<u>V</u>	<u>Q</u>	<u>W</u>	<u>L</u>					
					<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	<u>C</u>			
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	H	Y	F	D	Y
TGT	GCG	AGG	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	CAC	TAC	TTT	GAC	TAC
C	A	R	V	<u>Q</u>	<u>W</u>	<u>L</u>	<u>G</u>	-	H	F	D	Y
TGT	GCG	AGA	GTG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GGC</u>	TTA	AGA	---	CAC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>G</u>	A	E	-	N	F
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GGC</u>	GCA	GAA	---	AAC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	L	K	-	N	F
TGT	GCG	AGG	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	CTG	AAA	---	AAC	TTT
C	A	R	V	<u>Q</u>	<u>W</u>	<u>L</u>	<u>L</u>	L	E	-	R	F
TGT	GCG	AGA	GTT	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>TTA</u>	CTC	GAA	---	CGA	TTT
C	A	R	N	<u>Q</u>	<u>W</u>	<u>L</u>	<u>G</u>	L	D	Y	F	D
TGT	GCG	AGA	AAC	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GGT</u>	CTC	---	GAC	TAC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	R	T	-	S	F
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>	AGC	ACG	---	AGC	TTT
TGT	GCG	AGA	GAG	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>	AGG	ACG	---	AGC	TTT
C	A	R	E	<u>Q</u>	<u>W</u>							

4/16

FIG. 1 - 4

Set V1b,c,d

V _H 1-03				D6-19				J _H 4			
C	A	R	D/E	Y	F	D	Y				
TGT	GCG	AGA	GA	AC	TAC	TTT	GAC	TAC			
GG <u>GTA</u> <u>TAG</u> <u>CAG</u> <u>TGG</u> <u>CTG</u> <u>GTA</u> <u>C</u>											
V											
Q											
W											
L											
CTG											
GTA											
V											
L											
CTC											
S											
TCT											
L											
CTC											
V											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											
CTG											
GTA											
L											

7/16

FIG. 1 - 7

Set III.

V_R3-21
 C A R E/D
 TGT GCG AGA GA
 Y Y Y Y Y G M D V W G
 AT TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC

J_R6
 C A R D A N G M D V W G
 TGT GCG AGA GAT GCG AAT GGA ATG GAC GTC TGG GGC
 C A R D R N G M D V W G
 TGT GCG AGA GAT CGG AAC GGT ATG GAC GTC TGG GGC
 C A R D Q N G M D V W G
 TGT GCG AGA GAT CAA AAC GGT ATG GAC GTC TGG GGC
 C A S D R N G M D V W G
 TGT GCG AGC GAT CGA AAC GGT ATG GAC GTC TGG GGC
 C A R E P Y G M D V W G
 TGT GCG AGA GAG CCA TAC GGT ATG GAC GTC TGG GGC
 C A R D G S G M D V W G
 TGT GCG AGA GAT GGC TCC GGT ATG GAC GTC TGG GGC
 C A R D A N G M D V W G
 TGT GCG AGA GAT GCT AAC GGC ATG GAC GTC TGG GGC

ID28 ²
 AJ239379
 AF174100 sc77u-16 ⁹
 GN11 ⁸
 AJ389178
 AF299104 IF case 10 ¹⁰ U3

CLL282
 CLL175
 CLL412

8/16

FIG. 1 - 8

Set Vie

[illegible]

FIG. 1 - 9

9/16

V _H 1-02				D6-19				J _H 4							
C	A	R	D/E					AC	TTT	GAC	TAC				
TGT	GCG	AGA	GA												
		<u>V</u>	<u>Q</u>	<u>W</u>	<u>L</u>	<u>V</u>									
	<u>GG</u>	<u>GTA</u>	<u>TAG</u>	<u>CAG</u>	<u>TGG</u>	<u>CTG</u>	<u>GTA</u>								
C	A	R	E	Q	W	L	V	L	E	H	Y	F	D	Y	
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTT	GAG	CAC	TAC	TTT	GAC	TAC	CLL011
C	A	R	V	Q	W	L	G	L	R	-	H	F	D	Y	
TGT	GCG	AGA	GTC	CAG	TGG	CTG	GCC	TTA	AGA	---	CAC	TTT	GAC	TAC	CLL270
C	A	R	E	Q	W	L	G	A	E	-	N	F	D	Y	
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GGC	GCA	GAA	---	AAC	TTT	GAC	TAC	CLL266
C	A	R	E	Q	W	L	V	L	K	-	N	F	D	Y	
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTG	AAA	---	AAC	TTT	GAC	TAC	CLL340
C	A	R	V	Q	W	L	L	L	E	-	R	F	D	Y	
TGT	GCG	AGA	GTT	CAG	TGG	TTA	TTA	CTC	GAA	---	CGA	TTT	GAC	TAC	AJ239371
C	A	R	N	Q	W	L	G	L	D	-	Y	F	D	Y	CLL 3 ²
TGT	GCG	AGA	AAC	CAG	TGG	CTG	GGT	CTC	GAC	---	TAC	TTT	GAC	TAC	AJ487492
C	A	R	E	Q	W	L	V	R	T	-	S	F	D	Y	SMZL Tierens, A.M.
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GTA	AGG	ACG	---	AGC	TTT	GAC	TAC	U86787
C	A	R	E	Q	W	L	V	L	S	-	Y	F	D	Y	CLL-H2B ¹ U0
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTC	CTA	TCT	---	TAC	TTT	GAC	TAC	CLL336
C	A	R	E	Q	W	L	V	L	-	N	Y	F	D	Y	
TGT	GCG	AGG	GAG	CAG	TGG	CTG	GTA	CTT	---	AAC	TAC	TTT	GAC	TAC	CLL360
C	A	R	E	Q	W	L	A	L	K	-	P	F	D	Y	
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GCC	TTA	AAA	---	CCC	TTT	GAC	TAC	AF376961
C	A	R	K	Q	W	L	A	I	V	N	Y	F	D	Y	LAN Digheiro
TGT	GCG	AGA	AAG	CAG	TGG	CTG	GCC	ATC	GTC	AAC	TAC	TTT	GAC	TAC	L01278
C	A	R	E	Q	W	L	G	L	P	-	T	F	D	Y	CLL-412 ³
TGT	GCG	AGA	GAG	CAG	TGG	CTG	GGT	CTA	CCT	---	ACC	TTT	GAC	TAC	U86801 ⁴ U3/1
C	A	R	V	Q	W	L	G	L	T	G	P	N	D	Y	
TGT	GCT	AGG	GTT	CAG	TGG	CTG	GCG	CTG	ACG	GGG	CCG	AAT	GAC	TAC	U84176
C	A	R	G	Q	W	L	V	I	L	-	N	F	D	Y	KEM (VH1-46) ⁵ U0
TGT	GCG	AGG	GGA	CAG	TGG	CTG	GTC	ATC	CTA	---	AAC	TTT	GAC	TAC	U84162
C	A	R	D	Q	W	L	P	T	-	N	N	F	D	Y	BYR (VH1-46) ⁵ U0
TGT	GCG	AGA	GAT	CAG	TGG	CTG	CCC	ACG	---	AAC	AAC	TTT	GAC	TAC	AF376953
C	A	R	E	Q	W	L	V	L	S	-	H	F	D	Y	Digheiro PIQ U2
TGT	GCG	AGG	GAG	CAG	TGG	TTG	GTA	CTA	TCT	---	CAC	TTT	GAC	TAC	CLL154
C	A	R	Q	Q	W	L	G	G			D	Y	F	D	(VH1-18)
TGT	GCG	AGG	CAG	CAG	TGG	CTG	GGT	GGC			GAC	TAC	TTT	GAC	TAC
C	A	R	R	Q	W	L	A	L			G	H	F	D	Y
TGT	GCG	AGA	AGG	CAG	TGG	CTG	GCC	CTA			GGC	CAC	TTT	GAC	TAC

10/16

FIG. 2

Amino acid alignments of the H chain variable regions of all sequences in each Set

Set	CDR1	CDR2	CDR3
Set IV			
Germline	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDTAVYTCARD	YDYVWGSIYR	DAFDVWGQGTMTVTVSS
CELL068			GGD.....EN.....
CELL258			GGI.....FN.....
MF9			GGP.....FN.....
SKT			GGW...I...SN.....
CELL022			GGD.....FN.....I
ATE			GGN...I...SN.....V.....
Consensus	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDTAVYTCARGGDYDYVWGSIYRDAFDVWGQGTMTVTVSS		
Set VIII			
Germline	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDTAVYTCARD	DIVVVPAAI	YFYYGMDVWGQGTMTVTVSS
PS41			GG.....MS.....
UCM4			GA.....HG.....
G013			GG.....NR.....
Consensus	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDTAVYTCARGGDIVVVPAAI-YFYYGMDVWGQGTMTVTVSS		
Set V			
Germline	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDTAVYTCARD	IVRGVIT	YFYYGMDVWGQGTMTVTVSS
CELL561			AM.Q...QTY...YM...K.....
MF21			A...Y...X...K.....
RF22			G...Y...X...K.....
GH12			EG...Q...GI.....
FUE			S...Q...NVL.....
ID64			E...HLD...Y...X.....
SIN			V...SLD...Y...K...L.....
Consensus	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYALISWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITADKSTSTAYMELSSLRSEDTAVYTCARIVRGVITYFYYGMDVWGQGTMTVTVSS		
Set XII			
Germline	QVQLQNGAGLLKPSSETLSLTCAVYGSPFSYTHSWIRQPPGKGLWIGINHSSTINPBLKSRVITISVDTSKNQFSLKLSVTAADTAVYTCARG	VDPMV	YFYYGMDVWGQGTMTVTVSS
CELL183			YQ...PTIR...R.....
CELL240			A...I...YA...DVPR...AK.....
CELL342			NG...P.LKR...L.....
CELL48			AYP...P.RR...SVE...L.....
ID47			PP...DVTKR...F.....
Consensus	QVQLQNGAGLLKPSSETLSLTCAVYGSPFSYTHSWIRQPPGKGLWIGINHSSTINPBLKSRVITISVDTSKNQFSLKLSVTAADTAVYTCARGYDTPMKRRYYFYYGMDVWGQGTMTVTVSS		
Set VIA			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGINFNSGGTNYAQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL011			R...LKH.....
CELL266			S...GAEN.....
CELL270			V...GLER.....
CELL340			R...LKN.....
CLM3			V...LLER.....
HLV18			N...GLD.....
CLL-H2B			E...RTS.....
Consensus	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGINFNSGGTNYAQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARDQMLV-YFDYWGQGTMTVTVSS		
Set VIIb			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGINAGNGNTKYBQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL336			E...LS.....
CELL360			E...L.....
LAN			E...ALK-P.....
CLL-412			K...ALVN.....
POR			E...GLP-T.....
PIQ			PTN-N.....
Consensus	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGINAGNGNTKYBQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARDQMLV-YFDYWGQGTMTVTVSS		
Set VIC			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYISWVRQAPGQGLEWMGINISYNGSTNYAQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL154			E...LSH.....
Set VID			
Germline	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGINISYNGSTNYAQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
BYR			ILN.....
KRM			VGLTGN.....
Consensus	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGINISYNGSTNYAQKFGQGVITMDTSTSTAYMELSSLRSEDTAVYTCARGQMKKKKKEDYWGQGTMTVTVSS		
Set VIE			
Germline	QVQLVQSGAEVKKPGSLRISCRGSGYFTSYINISWVRQMPGKGLWNGRIDPDSYTNYSBPFQGHVITISADKSIISTAYLQWSSLRASDTAVYTCARDQMLV	YFDYWGQGTMTVTVSS	
CELL026			GGD.....
TRB			R...ALGH.....
CELL021			PQVY.....
ID38			LP.....
G014			E...TVTH.....
AG			LD.....
HOW			E...LSN.....
Consensus	QVQLVQSGAEVKKPGSLRISCRGSGYFTSYINISWVRQMPGKGLWNGRIDPDSYTNYSBPFQGHVITISADKSIISTAYLQWSSLRASDTAVYTCARDQMLVYFDYWGQGTMTVTVSS		

11/16
FIG. 3*Amino acid alignments of the L chain variable regions of all sequences in each Set.*

Set IV				
Germ line	EIVLTQSPFTLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLIYGASRRATGTPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSTPTFGQGTKVEIK	CDR1	CDR2	CDR3
CLL068
CLL258g.....
MF9
Consensus	EIVLTQSPFTLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLIYGASRRATGTPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSTPTFGQGTKVEIKl.....
Set VIII				
Germ line	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLIYDASRRATGTPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQRSNTFGPGTKVDIK	CDR1	CDR2	CDR3
GO13g.....
Set V				
Germ line	QSVLTQPPSLSGTPGQRTISCGSSGNTGNTVWYQQLPFTGTPAKLLIYNNQRFSGVDRFSGSKSGTSASLAIISGLQSEDEADYTCANWDDSLNGPFGGGKLTIVL	CDR1	CDR2	CDR3
RP22
GN12r.....
Consensus	QSVLTQPPSLSGTPGQRTISCGSSGNTGNTVWYQQLPFTGTPAKLLIYNNQRFSGVDRFSGSKSGTSASLAIISGLQSEDEADYTCANWDDSLNGPFGGGKLTIVLf.....
Set I				
Germ line	DVMTQSPFLSLPVTLGQFASISCRSSQSLVYSDGNTYLNWYQRPQSPRLIYKVENRDSGVDRFSGSGSGTDFTLTISRVEADGVYITCMQGTWTFPTFGQTKLEIK	CDR1	CDR2	CDR3
CLL183l.....
CLL240
CLL342v.....
Consensus	DVMTQSPFLSLPVTLGQFASISCRSSQSLVYSDGNTYLNWYQRPQSPRLIYKVENRDSGVDRFSGSGSGTDFTLTISRVEADGVYITCMQGTWTFPTFGQTKLEIKw.....
Set VI				
Germ line	DIQMTQSPFSLSLASGVDRVITTCRASQSISSYLNNWYQKPKAPKLLIYAASLIQSGVDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQSYSTPTFGQGTKVEIK	CDR1	CDR2	CDR3
Consensus	DIQMTQSPFSLSLASGVDRVITTCRASQSISSYLNNWYQKPKAPKLLIYAASLIQSGVDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQSYSTPTFGQGTKVEIKt.....
CLL011
CLL266k.....
CLL270l.....
CLL340l.....
CLL336l.....
CLL360s.....
CLL-412l.....
CLL154l.....
TFE
GO14l.....
Consensus	DIQMTQSPFSLSLASGVDRVITTCRASQSISSYLNNWYQKPKAPKLLIYAASLIQSGVDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQSYSTPTFGQGTKVEIKr.....

V _K 4-34	D5-5	J _H 6	V _K A17	J _K 1/2*
C A R G		Y Y Y	M Q G T H W P P	
tgt gcg aga gg		at tac tac tac	atg caa ggt aca cac tgg cct cc	
V D T A M V			W T F G	
gtg gat aca gct atg gtt ac			g tgg agg ttc ggc	
Y G . . P T I R . .		C L L 183		
. . . . a tac .g. . . . c. . cc a. . ga aga t				
. . . . Y A . . P V F R R . .		C L L 240		
. a tat .c. . . . t .c. . g. . t. . cgg cg. . . .				
. . . . W G . . P . L K R . .		C L L 342		
. c tgg .g. . . . c. . . . c. . . a aga				
. . . . A Y P . . P . V R R . .		C L L 4 B		
. ca tac cc. . . . c. c .gg agg				
. . . . F P . . D V I K R . .		I D 47		
. c ttc cc. a. g. . a. . g cg. . . .				
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15				

V _H 1-02	D6-19	JH4	VK 012/02	Jx1/2*
CARD/E		YFDY	QQSYSTPP	
tgt gag aga ga		ao tac ttt gaa tac	caa cag agt tac agt acc cat cc	
V * QWLV			WTFG	
gg gta tag cag tgg ctg gta o			g tgg acg tto gcc	

. L E H	CLL011 T
. tt gag a g ao
.	G A E - N	CLL266 K
. go gaa gaa
. . . V	G L R - H	CLL270
. go tta aga
.	L K - N	CLL340
. tg aaa
. . . V	L L E - R	CLL3
. tt . . . ta t . . . to gaa . . . cga
. . . N	G L D	slv18 (marginal zone lymphoma)
. a.o . . . gt . . . tc . . . g
. . . E	R T - S	CLL-H2B S
. agg acg . . . ag g
.	L S -	CLL336
. ta tot
.	L - N	CLL360
. tt . . . a
.	A L K - P	LAN
. oo tta aaa . . . oc
. . . K	A I V N	CLL-412
. co ata gtc a
.	P T - N N	PIQ
. oac acg . . . a
.	L S - H	CLL154
. ta tat . . . a
. . . G	I L - N	BYR
. ga oo atc cta . . . a
. . . V	G L T G P N	KEM
. t . . . g . . . tt . . . go . . . tg . . . acg . . . ggg . . . cog . . . aa
.	G G - D	CLL026
. g gt . . . ggc . . . g
. . . R	A L - G H	TRE
. ag cc . . . ta . . . gg . . . C
.	F G V - Y	CLL021
. a . . . t.c . . . go . . . gtg . . . t
.	L P -	ID38
. tt . . . oca
. . . E	I V T - H	GO14
. g co . . . a . . . gta . . . aot . . . a
.	L - D	AG
. g . . . tgg . . . g
. . . E	L S -	HOW

nucleotide sequence not available

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----

1	2	3	4	5	6	7	8	9	10	11	12	13
---	---	---	---	---	---	---	---	---	----	----	----	----